

# Crucial Roles of LncRNAs in Multiple Tumors

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## ABSTRACT

Long noncoding RNAs (lncRNAs) are a new class of regulators. LncRNAs are defined as endogenous transcribed RNA molecules with transcript length of >200 nt. Accumulating evidence has shown that lncRNAs are involved in many physiological processes such as cell cycle regulation, cell apoptosis and survival, cancer migration and metabolism.

## Keywords

Noncoding RNA; DNA; Pancreatic cancer; Apoptosis signals

## INTRODUCTION

The regulation and useful role of lncRNAs and the potential fundamental mechanism complicated in pancreatic cancer, outlined the roles of lncRNA in pancreatic cancer, and deliberated the potential possibility of lncRNAs as therapeutic targets in clinical practice. Furthermore, the potential of lncRNAs used as subtle biomarkers for diagnosis, prognosis and prediction of response to therapy in pancreatic cancer will also be discussed. Dysregulation of lncRNA in various cancers is considered as one of the leading forces during tumorigenesis. LncRNAs could interrelate specially with DNA and RNA, and changes in lncRNA expression levels could affect a broad spectrum of genes and phenotypic changes. Invasion and metastasis are the characteristics of pancreatic cancer. Metastasis-associated genes and proteins have been studied at the genetic level. It is reported that mutation of KRAS, p16, TP53 and SMAD4 are complicated in the metastatic process. However, the underlying mechanism is still controversial. In spite of the progress in surgical techniques, chemotherapy and radiotherapy, the survival of patients with pancreatic cancer has not substantially improved. One of the main reasons for the low overall survival is poor understanding of the difficult molecular mechanism in the progress of pancreatic cancer, counting changed cell physiology, dysfunction of cell growth and apoptosis signals, insensitivity to all cycle arrest signals, and evasion from programmed cell death.

## LNC-RNA IN CANCER

LncRNAs expression is significantly different between pancreatic cancer tissues and noncancerous tissues by a complementary DNA (cDNA) microarray questioning putative lncRNAs analysis. Moreover, the expression profiles of lncRNA between primary adenocarcinoma samples and metastatic samples collected from secondary tumors are also different. In total, 355 differentially expressed transcripts including 221 protein-coding mRNAs and 134 noncoding RNAs were found in a metastasis-associated signature. The expressions of oncogenic lncRNAs, such as HOTAIR, MALAT1 and H19, are higher in pancreatic cancers than that in the adjacent normal pancreatic tissue and are associated with more aggressive tumors, whereas the tumor suppressor lncRNAs expression such as gas5 and ENST00000480739 was unusually decreased in pancreatic cancer tissues compared with their corresponding nontumorous tissues. Abnormal expression level of lncRNA indicates the functional importance of lncRNA in pancreatic cancer tissue and their likely use as novel prognostic and diagnostic biomarkers.

## CONCLUSION

LncRNAs fulfill important functions in cancer initiation, progression, invasion and metastasis, as well as prognosis. In this review, we have discussed some examples of lncRNAs and the potential underlying mechanism involved in pancreatic cancer. LncRNAs may be used as diagnostic, prognostic biomarkers of

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cancer and provide a new strategy for pancreatic cancer treatment. However, there are still many challenges that remain to be solved. For example, the biological and molecular characteristics of most lncRNAs remain unknown and the mechanism of lncRNA in pancreatic cancer regulation is still not understood. More studies are needed to elucidate the association of lncRNAs and pancreatic cancer.

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